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CONTENTS/SUMMARIES

Summary: Microorganisms produce a spectrum of enzymes to degrade β-1,4-xylan, an abundant polysaccharide found in plant cell walls. These enzymes include β-1,4-xylanases, β-xylosidases, and various debranching enzymes that are all apparently required for the effective hydrolysis of the heterogeneous and highly branched substrate. To enhance their individual biodegradative capacity, microorganisms generally produce more than one xylanase. Each xylanase may have specialized functions that contribute significantly to the overall xylanolytic system of an organism. This is suggested by observations of cooperative interactions among multiple xylanases in the hydrolysis of complex xylans. Specialized functions of individual xylanases may be exploitable in biotechnological applications.

Summary: The genomes of many organisms contain genes that are transcribed divergently from closely spaced promoters. Such regions of divergent transcription occur in procaryotes, eucaryotes, and their viruses, with more than 60 examples to date found in organisms as diverse as bacteriophages and monkeys. The promoters in these regions occur in three arrangements: back-to-back, overlapping, and face-to-face. The regions also fall into three groups according to the gene products they encode. In one group, all of the gene products are catalytic or structural polypeptides. In another, all are regulatory macromolecules. In the third group, the gene products include both catalytic/structural and regulatory macromolecules. Most of the regulatory macromolecules are polypeptides, but some are ribonucleic acids. The implications of divergent promoter arrangements and their regulatory role are discussed.

Summary: Many bacterial pathogens evade the host immune system by altering the antigenic character of their surface molecules. Antigenic variation is defined here as the ability of a single strain of a microbe to express multiple antigenic variants of a cellular component, with the rate of antigenic variation being significantly higher than the mutation rate. Three systems that show high-frequency antigenic variation have been

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studied in detail: the pilin and protein II proteins of Neisseria gonorrhoeae, and the variable major protein of Borrelia hermsii. Antigenic variation of these three proteins rely on deoxyribonucleic acid recombination, although the mechanisms are different for each system. This review examines what is known about the mechanisms of antigenic variation in these bacteria and discusses other procaryotes that may undergo antigenic variation. Finally, the mechanisms govering bacterial antigenic variation are compared with the processes that lead to the generation of antibody diversity in eucaryotes.

Summary: The major purpose of the peptidoglycan wall of procaryotes is to provide a covering that can resist the tensile forces that tend to enlarge and deform the cell shape. The chemical nature of the murein is ideally suited for this purpose since it is covalently linked in two dimensions (the glycan and peptide directions). Thus, the entire wall constitutes a supermacromolecule, the sacculus. Because of this cross-linked structure, it is very strong, exceeding that of many metals and plastics. Nonetheless, the stresses arising from the hydrostatic pressure within the cells can be very large, and thus the structure must be protected from the initiation of tears or rips that would propagate to injure or destroy the cell. This is especially critical as the wall enlarges because autolytic events must occur during the process. Work over the past 10 years has shown that there are several strategies employed by different bacterial types. The major task of this review is the critical study of the available evidence of a variety of kinds, concerning the global aspects of wall growth. It has become clear that wall growth takes place by a nearly random process of insertion and cross-linking of new oligopeptidoglycan. The cell controls this process by arranging the sites for synthesis and autolysis. In addition, for cell division of the gram-negative organism to occur, the free energy requirement for polymerization must become locally altered. The second purpose of this review is to demonstrate how the technology of textiles and other material sciences can be pertinent, even critical, to the understanding of the procaryotic way of life.

Summary: The "nonsense" codons UAG (amber), UAA (ochre), and UGA (opal) function as translation termination signals in bacteria. Nonsense suppression (also called termination suppression) describes the phenomenon that amino acids are inserted into the growing polypeptide chain in response to these codons; thus, termination does not occur. This type of informational suppression is brought about by the existence of suppressor transfer ribonucleic acids (tRNAs) capable of recognizing the nonsense codon and inserting an amino acid into the growing polypeptide chain. Most suppressor mutations are located in the anticodon triplet of tRNAs, allowing reading of the nonsense codon. Extensive genetic and biochemical studies in the past few years have elucidated much of the detail of nonsense suppression in Escherichia coli. All naturally occurring tRNA suppressors derived by single base changes from wild-type tRNAs have now been found, and their sequences are known. In addition, gene construction by chemical synthesis or in vitro mutagenesis has given rise to entirely new suppressor tRNAs specific for many different amino acids. Many mutations have been characterized which affect the efficiency of suppression. These "antisuppressors" or "enhancers" of suppression include genes for enzymes involved in tRNA biosynthesis and genes for components of the protein-synthesizing machinery. In addition, the reading context of the messenger RNA also affects the efficiency of suppression. The usefulness of termination suppressors for elucidating various aspects of tRNA function, e.g., the role of modified nucleotides in tRNA, the recognition of tRNA by enzymes of tRNA metabolism (aminoacyl-tRNA synthetases, tRNA-modifying enzymes, and RNA-processing nucleases), and the accuracy of translation, is described. The availability of a diversity of suppressor tRNAs will be of great importance in studies of protein specificity and in protein engineering.

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Summary: We review various ways in which plasmids have been classified, especially their ordering into incompatibility groups, and we describe a new method for the identification and classification of plasmids, called replicon typing. In this method, specific deoxyribonucleic acid (DNA) probes derived from basic replicons of plasmids belonging to different incompatibility groups were used to test for the presence of similar basic replicons in plasmids by DNA-DNA hybridization. We describe the preparation of 19 probes derived from different replicons and evaluate their specificity. Their application to the typing of plasmids belonging to 27 different incompatibility groups is illustrated. For many plasmids, replicon typing and incompatibility grouping were equivalent, but for plasmids with multiple replicons or for groups of plasmids containing similar, but compatible replicons, replicon typing was less equivocal and more specific for identification and classification than incompatibility grouping. Moreover, replicon typing was simpler and faster to carry out than testing for incompatibility. Plasmids of medical importance, such as plasmids with genes for various virlence factors (for example, toxin production, adhesins, invasiveness, or drug resistance), frequently contain several basic replicons, and for their identification replicon typing was found to be especially useful.

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